

In the Claims:

The following claims will replace all prior versions and listings of claims in this application.

1 - 16. (Cancelled)

17. (Currently Amended) A method for modifying glycosylation structures on proteins expressed in a ~~lower eukaryote~~ eukaryotic host cell comprising: expressing a recombinant nucleic acid encoding an endomannosidase activity that is targeted to a vesicular compartment within the host cell ~~wherein the endomannosidase activity removes a composition comprising at least a glucose residue and one mannose residue on an oligosaccharide.~~

18. (Original) The method of claim 17 wherein the endomannosidase activity further comprises the activity of truncating $\text{Glc}_{1-3}\text{Man}_{9-5}\text{GlcNAc}_2$ to $\text{Man}_{8-4}\text{GlcNAc}_2$ wherein $\text{Glc}\alpha 1,3\text{Man}$, $\text{Glc}_2\alpha 1,3\text{Man}$ or $\text{Glc}_3\alpha 1,3\text{Man}$ are removed.

19. (Currently Amended) The method of claim 17 wherein the endomannosidase activity ~~comprises hydrolysis of a composition comprising~~ removes from a glucosylated glycan on proteins expressed in said host cell at least one glucose residue and at least one mannose residue ~~on glucosylated glycans.~~

20. (Currently Amended) The method of claim 17 wherein the endomannosidase ~~introduced are~~ is targeted to the endoplasmic reticulum, the early, medial, late Golgi[[,]] or trans Golgi network ~~or any vesicular compartment~~ within the host ~~organism~~ cell.

21. (Original) The method of claim 17 wherein the endomannosidase is of host origin but has been modified by mutation, promoter strength or copy number to enhance activity.

22. (Currently Amended) The method of claim [[17]] 35 wherein the endomannosidase is secreted.

23. (Currently Amended) The method of claim 17 wherein the host ~~cell~~ is a mammalian, plant, insect, fungal, yeast, algal or bacterial cell.

24. (Currently Amended) The method of claim 17 wherein the ~~lower~~ host cell is from a eukaryote [[is]] selected from the group consisting of ~~Pichia pastoris, Pichia finlandica, Pichia trehalophila, Pichia koelamae, Pichia membranaefaciens, Pichia opuntiae, Pichia thermotolerans, Pichia salietaria, Pichia guereuui, Pichia pijperi, Pichia stiptis, Pichia methanolica, Pichia sp., Saccharomyces cerevisiae, Saccharomyces sp., Hansenula polymorpha, Kluyveromyces sp., Kluyveromyces laetis, Candida albicans, Aspergillus nidulans, Aspergillus niger, Aspergillus oryzae, Trichoderma reesei, Chrysosporium lucknowense, Fusarium sp., Fusarium gramineum, Fusarium venenatum and Neurospora crassa.~~

25. (Currently Amended) [[A]] The method for ~~modifying glucosylated glycoproteins comprising introducing an endomannosidase activity in a lower eukaryotic host cell of claim 17~~ wherein ~~upon~~ expression of the endomannosidase activity modifies a glucosylated glycoprotein that has bypassed the [[ER]] endoplasmic reticulum.

26. (New) The method of claim 17, wherein the step of expressing said endomannosidase activity comprises

transforming a eukaryotic host cell with a nucleic acid molecule capable of expressing a polypeptide exhibiting endomannosidase activity, said nucleic acid molecule comprising or consisting of a nucleic acid sequence selected from the group consisting of: (a) SEQ ID NO: 1 or 3; (b) a nucleic acid sequence that is a degenerate variant of SEQ ID NO: 1 or 3; (c) a nucleic acid sequence at least 78% identical to SEQ ID NO: 1 or 3; (d) a nucleic acid sequence that encodes a polypeptide having the amino acid sequence of SEQ ID NO:2 or 4; (e) a nucleic acid sequence that encodes a polypeptide at least 77% identical to SEQ ID NO:2 or 4; (f) a nucleic acid sequence that hybridizes under stringent conditions to SEQ ID NO:1 or 3; and (g) a nucleic acid sequence comprising a fragment of any one of (a)-(f) that is at least 60 contiguous nucleotides in length and retains endomannosidase activity.

27. (New) The method of claim 26 wherein the endomannosidase activity has optimal activity at a pH between about 5.2 and about 7.2.

28. (New) The method of claim 26 wherein the endomannosidase activity has optimal activity at a pH of about pH 6.2.

29. (New) The method of claims 26 wherein the encoded polypeptide hydrolyzes at least one glucose residue and at least one mannose residue on a $\text{Glc}_{1-3}\text{Man}_5\text{GlcNAc}_2$, $\text{Glc}_{1-3}\text{Man}_6\text{GlcNAc}_2$, $\text{Glc}_{1-3}\text{Man}_7\text{GlcNAc}_2$, $\text{Glc}_{1-3}\text{Man}_8\text{GlcNAc}_2$, $\text{Glc}_{1-3}\text{Man}_9\text{GlcNAc}_2$ or glucosylated higher mannan glycan.

30. (New) A eukaryotic host cell that produces modified glycosylation structures on proteins according to the method of claim 17.

31. (New) The method of claim 24 wherein the *Pichia* sp. is selected from the group consisting of *Pichia pastoris*, *Pichia finlandica*, *Pichia trehalophila*, *Pichia koclamae*, *Pichia membranaefaciens*, *Pichia opuntiae*, *Pichia thermotolerans*, *Pichia salictaria*, *Pichia guercuum*, *Pichia pijperi*, *Pichia stiptis*, and *Pichia methanolica*.

32. (New) The method of claim 24 wherein the *Fusarium* sp. is selected from the group consisting of *Fusarium gramineum* and *Fusarium venenatum*.

33. (New) The method of claim 24 wherein the *Saccharomyces* sp. is *Saccharomyces cerevisiae*.

34. (New) The method of claim 24 wherein the *Kluyveromyces* sp. is *Kluyveromyces lactis*.

35. (New) A method for modifying glycosylation structures on proteins expressed in a lower eukaryotic host cell comprising expressing in the host cell a recombinant nucleic acid encoding an endomannosidase activity.

36. (New) The method of claim 35 wherein the endomannosidase activity further comprises the activity of truncating $\text{Glc}_{1-3}\text{Man}_{9-5}\text{GlcNAc}_2$ to $\text{Man}_{8-4}\text{GlcNAc}_2$ wherein $\text{Glc}\alpha 1,3\text{Man}$, $\text{Glc}_2\alpha 1,3\text{Man}$ or $\text{Glc}_3\alpha 1,3\text{Man}$ are removed.

37. (New) The method of claim 35 wherein the endomannosidase activity removes from a glucosylated glycan

on proteins expressed in said host cell at least one glucose residue and at least one mannose residue.

38. (New) The method of claim 35 wherein the endomannosidase is targeted to the endoplasmic reticulum, the early, medial, late Golgi, trans Golgi network or any vesicular compartment within the host cell.

39. (New) The method of claim 35 wherein the endomannosidase is of host origin but has been modified by mutation, promoter strength or copy number to enhance activity.

40. (New) The method of claim 35 wherein the host is a fungal, yeast or algal cell.

41. (New) The method of claim 35 wherein the lower eukaryotic host cell is from a eukaryote selected from the group consisting of *Pichia* sp., *Saccharomyces* sp., *Hansenula polymorpha*, *Kluyveromyces* sp., *Candida albicans*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, *Trichoderma reesei*, *Chrysosporium lucknowense*, *Fusarium* sp., and *Neurospora crassa*.

42. (New) The method of claim 41 wherein the *Pichia* sp. is selected from the group consisting of *Pichia pastoris*, *Pichia finlandica*, *Pichia trehalophila*, *Pichia koclamae*, *Pichia membranaefaciens*, *Pichia opuntiae*, *Pichia thermotolerans*, *Pichia salictaria*, *Pichia guercuum*, *Pichia pijperi*, *Pichia stiptis*, and *Pichia methanolica*.

43. (New) The method of claim 41 wherein the *Fusarium* sp. is selected from the group consisting of *Fusarium gramineum* and *Fusarium venenatum*.

44. (New) The method of claim 41 wherein the *Saccharomyces sp.* is *Saccharomyces cerevisiae*.

45. (New) The method of claim 41 wherein the *Kluyveromyces sp.* is *Kluyveromyces lactis*.

46. (New) The method of claim 41 wherein expression of the endomannosidase activity modifies a glucosylated glycoprotein that has bypassed the endoplasmic reticulum.

47. (New) The method of claim 35 wherein the step of expressing said endomannosidase activity comprises transforming the lower eukaryotic host cell with a nucleic acid molecule capable of expressing a polypeptide exhibiting endomannosidase activity, said nucleic acid molecule comprising or consisting of a nucleic acid sequence selected from the group consisting of: (a) SEQ ID NO: 1 or 3; (b) a nucleic acid sequence that is a degenerate variant of SEQ ID NO: 1 or 3; (c) a nucleic acid sequence at least 78% identical to SEQ ID NO: 1 or 3; (d) a nucleic acid sequence that encodes a polypeptide having the amino acid sequence of SEQ ID NO:2 or 4; (e) a nucleic acid sequence that encodes a polypeptide at least 77% identical to SEQ ID NO:2 or 4; (f) a nucleic acid sequence that hybridizes under stringent conditions to SEQ ID NO:1 or 3; and (g) a nucleic acid sequence comprising a fragment of any one of (a)-(f) that is at least 60 contiguous nucleotides in length and retains endomannosidase activity.

48. (New) The method of claim 47 wherein the endomannosidase activity has optimal activity at a pH between about 5.2 and about 7.2.

49. (New) The method of claim 47, wherein the endomannosidase activity has optimal activity at a pH of about pH 6.2.

50. (New) The method of claims 47, wherein the encoded polypeptide hydrolyzes at least one glucose residue and at least one mannose residue on a $\text{Glc}_{1-3}\text{Man}_5\text{GlcNAc}_2$, $\text{Glc}_{1-3}\text{Man}_6\text{GlcNAc}_2$, $\text{Glc}_{1-3}\text{Man}_7\text{GlcNAc}_2$, $\text{Glc}_{1-3}\text{Man}_8\text{GlcNAc}_2$, $\text{Glc}_{1-3}\text{Man}_9\text{GlcNAc}_2$ or glucosylated higher mannan glycan.

51. (New) A lower eukaryotic host cell that produces modified glycosylation structures on proteins according to the method of claim 35.